STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number: 101287

TO: Jeanine Goldberg
Location: cm1/12D11/12E12
Art Unit: 1634
Friday, August 15, 2003

Case Serial Number: 10/009897

From: Barb O'Bryen
Location: Biotech-Chem Library
CM1-6A05
Phone: 308-4291

barbara.obryen@uspto.gov

Search Notes

Jeanine,
For the Registry search, there were too many answers with the size limited to <100 nt, so I limited to <50 nt.
Barb

O'Bryen, Barbara

From: Goldberg, Jeanine
Sent: Monday, August 11, 2003 2:18 PM
To: O'Bryen, Barbara
Subject: 10/009897 ~~e.coli~~. HIV

Hello Barb-
Please place results on DISK.
Please search SEQ ID NO: 28 and 20 in both pending and commercial databases.
Please do a registry search for the primers of SEQ ID NO: 28 and 20 with less than 100 nucleotides.

THANK YOU
jeanine

Jeanine Enewold Goldberg
1634
CM1--12D11
Mailbox-- 12E12
306-5817

L9 ANSWER 87 OF 90 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1996:438786 CAPLUS
DOCUMENT NUMBER: 125:112561
TITLE: Biological phenotype of HIV type 2 isolates correlates with V3 genotype
AUTHOR(S): Albert, Jan; Staalhandske, Per; Marquina, Silvia; Karis, Jenny; Fouchier, Ron A. M.; Norrby, Erling; Chiodi, Francesca
CORPORATE SOURCE: Department Clinical Virology, Swedish Institute Infectious Disease Control, Stockholm, S-105 21, Swed.
SOURCE: AIDS Research and Human Retroviruses (1996), 12(9), 821-828
CODEN: ARHRE7; ISSN: 0889-2229
PUBLISHER: Liebert
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The biol. phenotype of HIV-2 isolates can be divided into two groups, rapid/high and slow/low, based on the ability to infect CD4+ tumor cell lines. Similar **differences** in the biol. phenotype of **HIV-1** isolates are largely determined by the charge of two specific amino acids in the V3 loop of the envelope protein gp120. In this study we have sequenced the V3 loop and flanking regions of 14 HIV-2 isolates from Guinea-Bissau and the Ivory Coast and correlated the results to the biol. phenotype of the isolates. The sequences were obtained by **PCR amplification** of DNA from peripheral blood mononuclear cells infected with the **different** isolates, followed by direct sequencing of the **amplified** products. Eleven other HIV-2 isolates with known V3 sequence and biol. phenotype were also included. Thirteen of the 14 new isolates were classified as **subtype** A of HIV-2 and one as **subtype** B. The V3 loop of rapid/high HIV-2 isolates differed significantly from slow/low isolates in that it was more heterogeneous in sequence and had higher net charge. Mutations at two specific amino acid positions (313 and 314), often to pos. charged amino acids, were also significantly associated with the rapid/high phenotype. There were no sequence **differences** between rapid/high and slow/low isolates in the regions that flank the V3 loop. Our findings indicate that there may be a high degree of similarity in the mol. features that underlie the biol. phenotypes of **HIV-1** and HIV-2 isolates.

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